

1. (Thrice Amended) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in a eucaryotic cell, comprising the step of introducing a chimeric DNA comprising the following operably linked parts:

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- a) a promoter, operative in said eucaryotic cell;
  - b) a DNA region, which when transcribed, yields an RNA molecule comprising an RNA region capable of forming an artificial hairpin RNA structure, wherein one of the annealing RNA sequences of the hairpin RNA structure comprises a sense sequence, essentially similar to at least 10 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and wherein the second of said annealing RNA sequences comprises an antisense sequence essentially similar to at least 10 consecutive nucleotides of the complement of at least part of said nucleotide sequence of said nucleic acid of interest, provided that said sense and said antisense sequence are not naturally occurring simultaneously in one RNA molecule; and optionally
  - c) a DNA region involved in transcription termination and polyadenylation.

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2. (Amended) A method for reducing the phenotypic expression of a nucleic acid of interest, which is normally capable of being expressed in a eucaryotic cell, comprising the step of introducing a chimeric DNA comprising the following operably linked parts:

- a) a promoter, operative in said eukaryotic cell;
- b) a DNA region, which when transcribed, yields an RNA molecule with a nucleotide sequence comprising

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- i) a sense nucleotide sequence including at least 10 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 10 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest; and
- ii) an antisense nucleotide sequence including at least 10 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 10 consecutive nucleotides of said sense nucleotide sequence;

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wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence such that said at least 10 consecutive nucleotides of the sense sequence basepair with said at least 10 consecutive nucleotides of the antisense sequence, provided that said sense sequence and said antisense sequence are not naturally occurring simultaneously in one RNA molecule; and optionally

- c) a DNA region involved in transcription termination and polyadenylation.

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4. (Amended) The method of claim 2, wherein said sense nucleotide sequence comprises at least about 550 consecutive nucleotides having between 75% and 100% sequence identity with at least about 550 consecutive nucleotides of the nucleotide sequence of said nucleic acid.

22. (Amended) A eucaryotic cell, comprising a nucleic acid of interest, which is normally capable of being phenotypically expressed, further comprising a chimeric DNA molecule comprising the following operably linked parts:

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- a) a promoter, operative in said eucaryotic cell;
  - b) a DNA region, which when transcribed, yields an RNA molecule with at least one RNA region with a nucleotide sequence comprising
    - i. a sense nucleotide sequence including at least 10 consecutive nucleotides having between 75 and 100% sequence identity with at least 10 consecutive nucleotides of the nucleotide sequence of the nucleic acid of interest; and
    - ii. an antisense nucleotide sequence including at least 10 consecutive nucleotides, having between about 75% to about 100% sequence identity with the complement of said at least 10 consecutive nucleotides of said sense nucleotide sequence;

wherein the RNA is capable of forming an artificial hairpin RNA structure with a double stranded RNA stem by base-pairing between the regions with sense and antisense nucleotide sequence, provided that said sense sequence and said antisense sequence are not naturally occurring simultaneously in one RNA molecule; and optionally

- c) a DNA region involved in transcription termination and polyadenylation.

Please add the following ~~new~~ claims:

43. (New) The method of claim 2, wherein said sense nucleotide sequence includes at least 20 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 20 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence.

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44. (New) The method of claim 2, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

45. (New) The method of ~~claim~~ 43, wherein said DNA region, which when transcribed yield said RNA molecule, ~~further~~ comprises an intron.

46. (New) The method of claim 45, wherein said intron is located between the DNA region encoding said sense nucleotide sequence and the DNA region encoding said antisense nucleotide sequence.

47. (New) The method of claim 43, wherein said eucaryotic cell is a plant cell.

48. (New) The method of claim 45, wherein said eucaryotic cell is a plant cell.

49. (New) The method of claim 44, wherein said DNA region, which when transcribed yield said RNA molecule, further comprises an intron.

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50. (New) The method of claim 49, wherein said intron is located between the DNA region encoding said sense nucleotide sequence and the DNA region encoding said antisense nucleotide sequence.

51. (New) The method of claim 44, wherein said eucaryotic cell is a plant cell.

52. (New) The method of claim 49, wherein said eucaryotic cell is a plant cell.

53. (New) The eucaryotic cell of claim 22, wherein said sense nucleotide sequence includes at least 20 consecutive nucleotides having between about 75 and about 100% sequence identity with at least 20 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 20 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 20 consecutive nucleotides of said sense nucleotide sequence.

54. (New) The eucaryotic cell of claim 22, wherein said sense nucleotide sequence includes at least 50 consecutive nucleotides having between about 75 and about 100% sequence

identity with at least 50 consecutive nucleotides of the nucleotide sequence of said nucleic acid of interest, and said antisense nucleotide sequence includes at least 50 consecutive nucleotides, having about 75% to about 100% sequence identity with the complement of said at least 50 consecutive nucleotides of said sense nucleotide sequence.

55. (New) The eucaryotic cell of claim 53, wherein said DNA region, which when transcribed yield said RNA molecule, further comprises an intron.

56. (New) The eucaryotic cell of claim 55, wherein said intron is located between the DNA region encoding said sense nucleotide sequence and the DNA region encoding said antisense nucleotide sequence.

57. (New) The eucaryotic cell of claim 54, wherein said DNA region, which when transcribed yield said RNA molecule, further comprises an intron.

58. (New) The eucaryotic cell of claim 57, wherein said intron is located between the DNA region encoding said sense nucleotide sequence and the DNA region encoding said antisense nucleotide sequence.

59. (New) The eucaryotic cell of claim 53, which is a plant cell.

60. (New) The eucaryotic cell of claim 55, which is a plant cell.

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conced* 61. (New) The eucaryotic cell of claim 54, which is a plant cell.

62. (New) The eucaryotic cell of claim 57, which is a plant cell.

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